

Art Unit: 1652

APPENDIX B

AI739096

LOCUS AI739096 368 bp mRNA linear EST 20-DEC-1999
DEFINITION w117h03.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2390549 3'
similar to TR:O35111 O35111 CTBAK. [2] TR:O54912 ;contains TAR1.t1
TAR1 repetitive element ;, mRNA sequence.
ACCESSION AI739096
VERSION AI739096.1 GI:5101077
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 368)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1184 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES
source Location/Qualifiers
1..368
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2390549"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Col6"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Col0 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 45.2%; Score 368; DB 9; Length 368;
Best Local Similarity 100.0%; Pred. No. 2.1e-163;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 AGGAAGTTCGGCTTCTCGGCCGAGGACTACCGCGAGCTGGAGCGCCTGGCGCTCCAGGCT 148
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Db 1 AGGAAGTTCGGCTTCTCGGCCGAGGACTACCGCGAGCTGGAGCGCCTGGCGCTCCAGGCT 60
|||
Qy 149 GAGCCCCACCGCGCCGGCCGAGTGGGAAGTTCCCGGCTCCTTCTACTTCGCCATCACC 208
|||
Db 61 GAGCCCCACCGCGCCGGCCGAGTGGGAAGTTCCCGGCTCCTTCTACTTCGCCATCACC 120
|||
Qy 209 GTCATCACTACCATCGAGTACGGCCACGCCGCGCGGGTACGGACTCCGGCAAGGTCTTC 268
|||
Db 121 GTCATCACTACCATCGAGTACGGCCACGCCGCGCGGGTACGGACTCCGGCAAGGTCTTC 180
|||
Qy 269 TGCATGTTCTACGCGCTCCTGGGCATCCCGCTGACGCTGGTCACTTTCAGAGCCTGGGC 328
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      |||
Db      181 TGCATGTTCTACGCGCTCCTGGGCATCCCGCTGACGCTGGTCACTTTCAGAGCCTGGGC 240
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Qy      329 GAACGGCTGAACGCGGTGGTGCGGCGCCTCCTGTTGGCGGCCAAGTGCTGCCTGGGCCTG 388
      |||
Db      241 GAACGGCTGAACGCGGTGGTGCGGCGCCTCCTGTTGGCGGCCAAGTGCTGCCTGGGCCTG 300
      |||
Qy      389 CGGTGGACGTGCGTGTCCACGGAGAACCTGGTGGTGGCCGGGCTGCTGGCGTGTGCCGCC 448
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Db      301 CGGTGGACGTGCGTGTCCACGGAGAACCTGGTGGTGGCCGGGCTGCTGGCGTGTGCCGCC 360
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Qy      449 ACCCTGGC 456
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Db      361 ACCCTGGC 368

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